OM protein - protein search, using sw model

Run on: December 6, 2005, 18:05:17 ; Search time 133.243 Seconds
                                            (without alignments)
                                            1490.508 Million cell updates/sec

Title: US-10-782-002-35
Perfect score: 2505
Sequence: 1 MMMKQYLQYLAAALPLVGLA.........DAQVVWSNIRFGPIGSTYDF 452

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_21:*
          1:   geneseqp1980s:*
          2:   geneseqp1990s:*
          3:   geneseqp2000s:*
          4:   geneseqp2001s:*
          5:   geneseqp2002s:*
          6:   geneseqp2003as:*
          7:   geneseqp2003bs:*
          8:   geneseqp2004s:*
          9:   geneseqp2005s:*

                    GenCore version 5.1.6
              Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2005, 18:09:07 ; Search time 26.1361 Seconds
                                            (without alignments)
                                            1663.984 Million cell updates/sec

Title: US-10-782-002-35
Perfect score: 2505
Sequence: 1 MMMKQYLQYLAAALPLVGLA.........DAQVVWSNIRFGPIGSTYDF 452

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
          1:   pir1:*
          2:   pir2:*

```
                    3:   pir3:*
                    4:   pir4:*


                         GenCore version 5.1.6
                  Copyright (c) 1993 - 2005  Compugen Ltd.


OM protein - protein search, using sw model

Run on:            December  6, 2005, 18:06:47 ; Search time 157.841 Seconds
                                            (without alignments)
                                            2020.377 Million cell updates/sec

Title:             US-10-782-002-35
Perfect score:     2505
Sequence:          1 MMMKQYLQYLAAALPLVGLA.........DAQVVWSNIRFGPIGSTYDF 452

Scoring table:     BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched:          2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:       2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :         UniProt_05.80:*
                   1:   uniprot_sprot:*
                   2:   uniprot_trembl:*


                         GenCore version 5.1.6
                  Copyright (c) 1993 - 2005  Compugen Ltd.


OM protein - protein search, using sw model

Run on:            December  6, 2005, 18:05:17 ; Search time 126.757 Seconds
                                            (without alignments)
                                            1490.508 Million cell updates/sec

Title:             US-10-782-002-35_COPY_23_452
Perfect score:     2398
Sequence:          1 QRAGNETPENHPPLTWQRCT.........DAQVVWSNIRFGPIGSTYDF 430

Scoring table:     BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched:          2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters:       2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :         A_Geneseq_21:*
                   1:   geneseqp1980s:*
                   2:   geneseqp1990s:*
                   3:   geneseqp2000s:*
```

```
                    4:  geneseqp2001s:*
                    5:  geneseqp2002s:*
                    6:  geneseqp2003as:*
                    7:  geneseqp2003bs:*
                    8:  geneseqp2004s:*
                    9:  geneseqp2005s:*
```

OM protein - protein search, using sw model

Run on: December 6, 2005, 18:09:07 ; Search time 24.8639 Seconds
                                              (without alignments)
                                   1663.984 Million cell updates/sec

Title: US-10-782-002-35_COPY_23_452
Perfect score: 2398
Sequence: 1 QRAGNETPENHPPLTWQRCT.........DAQVVWSNIRFGPIGSTYDF 430

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
                   1: pir1:*
                   2: pir2:*
                   3: pir3:*
                   4: pir4:*

OM protein - protein search, using sw model

Run on: December 6, 2005, 18:06:47 ; Search time 150.159 Seconds
                                              (without alignments)
                                   2020.377 Million cell updates/sec

Title: US-10-782-002-35_COPY_23_452
Perfect score: 2398
Sequence: 1 QRAGNETPENHPPLTWQRCT.........DAQVVWSNIRFGPIGSTYDF 430

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%

Listing first 45 summaries

Database :   UniProt_05.80:*
            1:   uniprot_sprot:*
            2:   uniprot_trembl:*